

# 2  
OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/023,617

DATE: 01/15/2002  
TIME: 18:02:44

Input Set : A:\10448-123001.TXT  
Output Set: N:\CRF3\01152002\J023617.raw

ENTERED

4 <110> APPLICANT: Bandaru, Rajasekhar  
5 Meyers, Rachel A.  
7 <120> TITLE OF INVENTION: 55562 AND 21617, NOVEL HUMAN PROTEINS  
8 AND METHODS OF USE THEREOF  
11 <130> FILE REFERENCE: 10448-123001  
13 <140> CURRENT APPLICATION NUMBER: US/10/023,617  
13 <141> CURRENT FILING DATE: 2001-12-18  
13 <150> PRIOR APPLICATION NUMBER: 60/256,249  
14 <151> PRIOR FILING DATE: 2000-12-18  
16 <150> PRIOR APPLICATION NUMBER: 60/256,405  
17 <151> PRIOR FILING DATE: 2000-12-18  
19 <160> NUMBER OF SEQ ID NOS: 10  
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
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24 <211> LENGTH: 3624  
25 <212> TYPE: DNA  
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28 <220> FEATURE:  
29 <221> NAME/KEY: CDS  
30 <222> LOCATION: (339)...(1361)  
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35 ccggggccac agcgccgagc cccggcggga gtggccccgc gcaggcaggg agcggcgccg 180  
36 cgcactccaa cccggcgggc acctcggggg cgggcgcggg ggcgcggc ctcgtccgg 240  
37 cctctgtgac aagcgccccc gagccggggag cccgattgcc gggctcgaaa tggcgccgaa 300  
38 cgcaggcaact gggctcggtc gggggcccccgg gcgtcgcg atg aac atc gtg gtg gag 356  
39 Met Asn Ile Val Val Glu  
40 1 5  
42 ttc ttc gtg gtc act ttc aaa gtg ctc tgg gcg ttc gtg ctg gcc gcg 404  
43 Phe Phe Val Val Thr Phe Lys Val Leu Trp Ala Phe Val Leu Ala Ala  
44 10 15 20  
46 gcg cgc tgg ctg gtg cgg ccc aag gag aag agc gtg gcg ggc cag gtg 452  
47 Ala Arg Trp Leu Val Arg Pro Lys Glu Lys Ser Val Ala Gly Gln Val  
48 25 30 35  
50 tgc ctc atc acc ggc gcc ggc agc ggc ctg ggc cgc ctc ttc gcg ctg 500  
51 Cys Leu Ile Thr Gly Ala Gly Ser Gly Leu Gly Arg Leu Phe Ala Leu  
52 40 45 50  
54 gag ttc gcc cgg cgt cgg gcg ctg ctg gtg ctg tgg gac atc aac acg 548  
55 Glu Phe Ala Arg Arg Ala Leu Leu Val Leu Trp Asp Ile Asn Thr  
56 55 60 65 70  
58 caa agc aac gag gag acg gct ggc atg gtg cgc cac atc tac cgc gac 596  
59 Gln Ser Asn Glu Glu Thr Ala Gly Met Val Arg His Ile Tyr Arg Asp  
60 75 80 85  
62 ctg gag gcg gcc gac gcc gct gcg ctg caa gct ggg aat ggt gag gaa 644  
63 Leu Glu Ala Ala Asp Ala Ala Leu Gln Ala Gly Asn Gly Glu Glu  
64 90 95 100

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68	105							110				115					
70	gtg	ggg	aag	agg	gag	aac	gtc	tac	ctg	acg	gct	gaa	aga	gtc	cgc	aag	740
71	Val	Gly	Lys	Arg	Glu	Asn	Val	Tyr	Leu	Thr	Ala	Glu	Arg	Val	Arg	Lys	
72	120							125			130						
74	gag	gtt	ggc	gaa	gtc	tca	gtc	ctg	gtc	aat	aat	gct	ggt	gtg	gtc	tct	788
75	Glu	Val	Gly	Glu	Val	Ser	Val	Leu	Val	Asn	Asn	Ala	Gly	Val	Val	Ser	
76	135							140			145			150			
78	ggg	cat	cac	ctt	ctg	gaa	tgt	cct	gat	gag	ctc	att	gag	aga	acc	atg	836
79	Gly	His	His	Leu	Leu	Glu	Cys	Pro	Asp	Glu	Leu	Ile	Glu	Arg	Thr	Met	
80	155							160			165						
82	atg	gtc	aat	tgc	cat	gca	cac	ttc	tgg	acc	act	aag	gct	ttt	cct	cct	884
83	Met	Val	Asn	Cys	His	Ala	His	Phe	Trp	Thr	Thr	Lys	Ala	Phe	Leu	Pro	
84	170							175			180						
86	acg	atg	ctg	gag	att	aat	cat	gtt	cat	att	gtg	aca	gtt	gca	agt	tcc	932
87	Thr	Met	Leu	Glu	Ile	Asn	His	Gly	His	Ile	Val	Thr	Val	Ala	Ser	Ser	
88	185							190			195						
90	ttg	gga	ttg	tgc	agt	act	gcc	gga	gtt	gag	gat	tac	tgt	gcc	agt	aaa	980
91	Leu	Gly	Leu	Phe	Ser	Thr	Ala	Gly	Val	Glu	Asp	Tyr	Cys	Ala	Ser	Lys	
92	200							205			210						
94	ttt	gga	gtt	gtg	ggt	ttt	cat	gaa	tcc	ctg	agc	cat	gaa	cta	aag	gct	1028
95	Phe	Gly	Val	Val	Gly	Phe	His	Glu	Ser	Leu	Ser	His	Glu	Leu	Lys	Ala	
96	215							220			225			230			
98	gct	gaa	aag	gat	gga	att	aaa	aca	acc	ttg	gtt	tgc	cct	tat	ctt	gta	1076
99	Ala	Glu	Lys	Asp	Gly	Ile	Lys	Thr	Thr	Leu	Val	Cys	Pro	Tyr	Leu	Val	
100	235							240			245						
102	gac	act	ggc	atg	ttc	aga	ggc	tgc	cga	atc	agg	aaa	gaa	att	gag	cct	1124
103	Asp	Thr	Gly	Met	Phe	Arg	Gly	Cys	Arg	Ile	Arg	Lys	Glu	Ile	Glu	Pro	
104	250							255			260						
106	ttt	ctg	cca	cct	ctg	aag	cct	gat	tac	tgt	gtg	aag	cag	gcc	atg	aag	1172
107	Phe	Leu	Pro	Pro	Leu	Lys	Pro	Asp	Tyr	Cys	Val	Lys	Gln	Ala	Met	Lys	
108	265							270			275						
110	gcc	atc	ctc	act	gac	cag	ccc	atg	atc	tgc	act	ccc	cgc	ctc	atg	tac	1220
111	Ala	Ile	Leu	Thr	Asp	Gln	Pro	Met	Ile	Cys	Thr	Pro	Arg	Leu	Met	Tyr	
112	280							285			290						
114	atc	gtg	acc	tgc	atg	aag	agc	atc	cta	cca	ttt	gaa	gca	gtt	gtg	tgc	1268
115	Ile	Val	Thr	Phe	Met	Lys	Ser	Ile	Leu	Pro	Phe	Glu	Ala	Val	Val	Cys	
116	295							300			305			310			
118	atg	tat	cgg	tgc	cta	gga	gcf	gac	aag	tgt	atg	tac	ccc	ttt	att	gct	1316
119	Met	Tyr	Arg	Phe	Leu	Gly	Ala	Asp	Lys	Cys	Met	Tyr	Pro	Phe	Ile	Ala	
120	315							320			325						
122	caa	aga	aag	caa	gcc	aca	aac	aat	aat	gaa	gca	aaa	aat	gga	atc		1361
123	Gln	Arg	Lys	Gln	Ala	Thr	Asn	Asn	Asn	Glu	Ala	Lys	Asn	Gly	Ile		
124	330							335			340						
126	taagaatctt	tttgttatgga	atattacttc	tatcagaaga	tgtatcaagat	gtttcagtcc											1421
127	agtgcacatc	agcatttgctg	acattttatg	gattctaaac	tttgtttgtt	tcttttttaa											1481
128	atcaactttt	aaaaaaaata	aagtgtaaat	taaccgacta	gagtacttgg	aaaatgtgat											1541
129	cagtacaagt	gaaccttaggt	tgttgccaaac	agggtccttt	taggcagaac	ccagaaacca											1601

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130	gtcaaatctg	tagagaagca	gtgtgacatc	ttcaggttac	cattatttt	taatgagcag	1661										
131	gaagtctaga	aatgataact	agactgtatg	tttcatgtgt	gtatTTTC	agaattccca	1721										
132	gagtttactc	attctgtta	ttaaactcta	gccagttgac	atcttcgcaa	tttcaaggac	1781										
133	tgatagtgt	gtatTTTCTC	acgtttctta	agtttccgtt	ttgcaaggcc	taggtgactt	1841										
134	tttcatgggt	tttgcgtatgtt	tagctcttt	gaaaaggaat	tttgcgtatct	ccatcaactg	1901										
135	aagtaaatga	tgtctgagtg	ttacagtwwa	ggtgaccaag	tctctttctt	aaagtccaa	1961										
136	tgactaaagt	attagttgaa	ttttttttt	ttttttgtat	ggagtctcgc	tctgtcacca	2021										
137	ggctggagtg	cagtagcaca	atcacggctc	actgcaatct	ctgcctccr	gtttcaagtg	2081										
138	attctgctgt	ctcagccctcc	caagtagctg	ggactacagg	catgcgcccc	cacgcccagc	2141										
139	taatTTTGT	atTTTtagta	gagacgggtt	ttcaccatgt	tggtcaggat	ggtctccatc	2201										
140	tcttgacatt	gtgatccacc	tgcctcgccc	tcccaaagtg	ctgggattac	aggcatgagc	2261										
141	cactgcaccc	agccttgaat	ttttaatttt	atctctgata	tacttcatta	agtgtctgga	2321										
142	gacctaatta	tcctaaaaga	tcatacattt	tctacctatg	aattttgtg	catacagaaa	2381										
143	gtgcccttcc	ctcaggaagt	tgctgtgtt	cattttttg	gatggactct	tatctagaat	2441										
144	acatagcagc	tctgcaaaaga	aacagttttt	aaaaatggga	acttctacat	tgaaaagtcc	2501										
145	ccatTTTGT	gccttgcata	attagtggaa	ggaagaaatc	ttattctatg	gcatatgtat	2561										
146	ggaagggtgt	aaagattctt	ttgaaaggtt	tatttcacatt	gtagaacacgc	aaatgacatt	2621										
147	tttacagtat	ttttttgtaa	agccaaactat	tttgcgtt	gaatttggta	tatgtgtatt	2681										
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149	aaatgactat	aaacttattat	gtgattgtt	ttttttttttt	ttttttttttt	ttttttttttt	2801										
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159	ctgaagggtt	tcaacaatgc	caggtgggg	cagatatact	cagagattat	ccaggtctgc	3401										
160	ctcccagcga	gcctggagta	caccagaccc	tcctagagaa	atctgttata	atttacaaac	3461										
161	ccacttatcc	acctaaaac	tgaggaaagt	cgttttaca	tctaattttt	ttttgtgtt	3521										
162	ttataactt	aaccttattt	tattttttt	ttttttttttt	ttttttttttt	ttttttttttt	3581										
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174						20					25				30		
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177	Gly	Arg	Leu	Phe	Ala	Leu	Glu	Phe	Ala	Arg	Arg	Arg	Ala	Leu	Leu	Val	
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183	Ala	Gly	Asn	Gly	Glu	Glu	Glu	Ile	Leu	Pro	His	Cys	Asn	Leu	Gln	Val
184				100					105					110		
185	Phe	Thr	Tyr	Thr	Cys	Asp	Val	Gly	Lys	Arg	Glu	Asn	Val	Tyr	Leu	Thr
186					115			120					125			
187	Ala	Glu	Arg	Val	Arg	Lys	Glu	Val	Gly	Glu	Val	Ser	Val	Leu	Val	Asn
188					130			135				140				
189	Asn	Ala	Gly	Val	Val	Ser	Gly	His	His	Leu	Leu	Glu	Cys	Pro	Asp	Glu
190	145				145		150			155				160		
191	Leu	Ile	Glu	Arg	Thr	Met	Met	Val	Asn	Cys	His	Ala	His	Phe	Trp	Thr
192					165			170			175					
193	Thr	Lys	Ala	Phe	Leu	Pro	Thr	Met	Leu	Glu	Ile	Asn	His	Gly	His	Ile
194					180			185			190					
195	Val	Thr	Val	Ala	Ser	Ser	Leu	Gly	Leu	Phe	Ser	Thr	Ala	Gly	Val	Glu
196					195			200			205					
197	Asp	Tyr	Cys	Ala	Ser	Lys	Phe	Gly	Val	Val	Gly	Phe	His	Glu	Ser	Leu
198					210			215			220					
199	Ser	His	Glu	Leu	Lys	Ala	Ala	Glu	Lys	Asp	Gly	Ile	Lys	Thr	Thr	Leu
200	225				225			230			235			240		
201	Val	Cys	Pro	Tyr	Leu	Val	Asp	Thr	Gly	Met	Phe	Arg	Gly	Cys	Arg	Ile
202					245			250			255					
203	Arg	Lys	Glu	Ile	Glu	Pro	Phe	Leu	Pro	Pro	Leu	Lys	Pro	Asp	Tyr	Cys
204					260			265			270					
205	Val	Lys	Gln	Ala	Met	Lys	Ala	Ile	Leu	Thr	Asp	Gln	Pro	Met	Ile	Cys
206					275			280			285					
207	Thr	Pro	Arg	Leu	Met	Tyr	Ile	Val	Thr	Phe	Met	Lys	Ser	Ile	Leu	Pro
208					290			295			300					
209	Phe	Glu	Ala	Val	Val	Cys	Met	Tyr	Arg	Phe	Leu	Gly	Ala	Asp	Lys	Cys
210	305				305			310			315			320		
211	Met	Tyr	Pro	Phe	Ile	Ala	Gln	Arg	Lys	Gln	Ala	Thr	Asn	Asn	Asn	Glu
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224	atcacccggc	ccggcagcgg	cctggccgc	ctcttcgcgc	tggagttcgc	ccgcgtcgg								180		
225	gcgctgtgg	tgcgtgtgg	catcaacacg	caaagcaacg	aggagacggc	tggcatgtgg								240		
226	cggccacatct	accgcgaccc	ggaggcggcc	gacccgcgt	cgctgcgaac	tggaaatgg								300		
227	gaggaagaaa	ttctgcccc	ctgttaactt	caggtttta	cctacaccc	tgacgtgggg								360		
228	aagaggggaga	acgtctaccc	gacggctgaa	agagtccgca	aggagggttgg	cgaagtctca								420		
229	gtcctggtca	ataatgtgg	tgtggtctt	gggcattacc	ttctggaaatg	tcctgtatgg								480		
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234	gtttgccctt	atcttgtaga	cactggcatg	ttcagaggct	gccgaatcag	gaaagaaaatt	780
235	gagccctttc	tgccacactt	gaagcctgtat	tacttgtga	agcaggccat	gaaggccatc	840
236	ctcaactgacc	agccccatgtat	ctgcactccc	cgcctcatgt	acatcggtac	cttcatgaag	900
237	agcatccat	catttgaagc	agtttgtgtc	atgtatcggt	tccttaggagc	ggacaagtgt	960
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253	cggatacaccc	ttgcgaagaa	tgcgcactc	tccgcactc	atccccact	caccggcacc	180
254	cgtctaaacct	tcagcctgaa	atttcctcc	gaaggaagca	gagcagagga	agaactacca	240
255	agtgcgtacac	tcaaaggctg	cgtcgca	gagcgcgacc	tccaaactga	ggcattttg	300
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257	tatcacatg	accacttcc	cgaaagc	cgccatc	ggcatttttgc	caaatttttgc	408
258							
	Met	Thr	Ser	Arg	Arg	Pro	Ala
	1	5	10				
261	cct	ggg	ttg	agg	cgg	agg	456
262	Pro	Gly	Leu	Arg	Arg	Arg	Arg
263	15	20	25	30			
265	ctg	agg	cag	gac	ccg	cag	504
266	Leu	Arg	Gln	Asp	Pro	Gln	Ser
267	35	40	45				
269	gca	gta	gaa	cta	gtc	gag	552
270	Ala	Val	Glu	Leu	Asp	Ser	Glu
271	50	55	60				
273	tac	caa	gag	ggg	att	gat	600
274	Tyr	Gln	Glu	Ile	Asp	Leu	Leu
275	65	70	75				
277	gat	aat	act	aag	aga	tgt	648
278	Asp	Asn	Thr	Lys	Arg	Cys	Asn
279	80	85	90				
281	gac	aga	gct	gaa	aac	ata	696
282	Asp	Arg	Ala	Glu	Asn	Ile	Lys
283	95	100	105	110			
285	gga	aaa	tat	cac	aag	caa	744
286	Gly	Lys	Tyr	His	Lys	Gln	Ile
287	115	120	125				
289	agt	tat	gag	tca	ctt	ttt	792
290	Ser	Tyr	Glu	Ser	Leu	Phe	Arg
291	130	135	140				

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date